

XX

PT	Nucleic acid encoding gibberellin inhibitor GAI and related			
PT	antisense sequences - used to create tall, or particularly, dwarf			
PT	plants, especially crops such as maize, rice and wheat			
XX				
PS	Claim 1; Fig 4; 76pp; English.			
XX				
CC	The present sequence is the Arabidopsis thaliana gibberellin			
CC	insensitivity (gai) gene product (GAI), the expression of which			
CC	inhibits plant growth. However the inhibition is antagonised by			
CC	gibberellin (GA), while gai expression confers a dwarf phenotype			
CC	that is insensitive to GA. Manipulating gai and GAI expression can			
CC	produce tall or dwarf plants, particularly the latter for increased			
CC	resistance to lodging and increased yield. It may also allow			
CC	regulation of flowering, i.e. plants remain in the vegetative state			
CC	until treated with GA, useful to inhibit bolting in spinach and			
CC	lettuce. GAI can be used to raise specific antibodies for			
CC	identifying homologous proteins or genes in other species. gai			
CC	fragments can also be used as probes or primers to identify and			
CC	clone related sequences, or in the preparation of antisense or			
CC	sense expression regulating (co-suppressing) sequences. Rice plants			
CC	that express GAI may be resistant to Bakane disease. Manipulation			
CC	of gai and GAI makes it possible to tailor the degree of dwarfism			
CC	and GA sensitivity to particular crops or situations.			
XX				
SQ	Sequence 532 AA;			
Query Match 100.0%; Score 2758; DB 18; Length 532;				
Best Local Similarity 100.0%; Pred. No. 1.5e-256;				
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MKRDRHHHQDKTKMMNEEDGNGMDLLAVLGKVKRSSEMDVAQKLEQLEVMNSVQ	60	
DB	1	mkrdrhhhhqdktkmmneeedgngmdellavlgvkvrsemdvqkleglevmnsnvq	60	
QY	61	EDDLISOLATEVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASS	120	
DB	61	eddlisqlatetvhympaeltytwldsmldclnppssnaeydikaipgdailnqfaidsass	120	
QY	121	SNQGGGGDTYTNRLKCSNGVWETTTATAESTRHVVLVDSQENGVRVLHALLACAEAVQ	180	
DB	121	snqggggdtytnrkcsngvvtettataestrhvvlvdsqengvrvlhallacaeavq	180	
QY	181	KENLTVAEALVKQIGFLAVSOGAMRKVATYFAEALARRIYRLSPSQPIDHSLDITLQM	240	
DB	181	kentvaealvkqigflavsqigamrkvatyfaealarriyrlspsgpidhslsdtlqm	240	
QY	241	HFYETCPYLKFAHTANOALEAFQKKRVHVIDFMSOGLQWPALMOALALRPGGPPVF	300	
DB	241	hfyetcpylkfahftanqaleafqgkkrvividfmsqglqwpalmqalalrpggppvf	300	
QY	301	RLTGIGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYRGFVANTLADLASMLELRPSEIE	360	
DB	301	rltligppapdnfdylhevvgcklahlaeahivefeyrgfvantladlasmlelrpseie	360	
QY	361	SVANVSFELHKLGRPAIDKVLGVVNIQIKPEITFTVVEQESNHSPIFLDRFTESLHYI	420	
DB	361	svanvsfelhklgrpaiddkvlgvvnqikpeiftvveqesnhspifldrfteslhyi	420	
QY	421	STLFDLSLEGVPSGQDKVMSEYVLGKICNVVACDGPDRVERHETLSQWRNRFSGAGFAA	480	
DB	421	stlfdlslegvpsgqdkvmsevylgkicnvvacdgpdrverheltsqwrnrfsgagfaa	480	
QY	481	HIGSNAFKQASMLIALFNGGEGYRVESDGCMLGWHTRPLIATSAWKLSN 532		
DB	481	higsnafkqasmllalfnggegryrveesdgcmlgwhtrplriatsawklstn 532		
RESULT 2				
AAE02545				
ID	AAE02545 standard; Protein: 532 AA.			
XX				
AC	AAE02545;			

XX	10-AUG-2001	(first entry)	
XX	A. thaliana transcription factor G308.		
XX			
KW	Plant transcription factor; phenotype; sugar sensing characteristic;		
KW	transgenic plant; plant yield; growth; germination; photosynthesis;		
KW	glyoxylate metabolism; respiration; pathogen response; wounding response;		
KW	cell cycle regulation; pigmentation; flowering; senescence; physiology;		
XX	storage organ; metabolism.		
OS	Arabidopsis thaliana.		
XX			
FT	Key	Location/Qualifiers	
FT	Domain	270..274	
FT	/note= "Conserved domain"		
PN	WO200135725-A1.		
XX			
PD	25-MAY-2001.		
XX			
PF	14-NOV-2000; 2000WO-US31414.		
XX			
PR	17-NOV-1999; 99US-0166228.		
PR	17-APR-2000; 2000US-0197899.		
PR	22-AUG-2000; 2000US-0227439.		
XX			
PA	(MEND-) MENDEL BIOTECHNOLOGY INC.		
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PA	(HEAR/) HEARD J.		
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PA	(SAMA/) SAMAHA R.		
XX			
PI	Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;		
PI	Yu G, Samaha R;		
XX			
DR	WPI; 2001-335977/35.		
DR	N-PSDB; AAD06646.		
XX			
PT	Nucleic acids encoding plant transcription factor polypeptides, useful		
PT	for altering the sugar sensing characteristics of plants and increasing		
PT	yield, e.g. corn, potato and cotton plants -		
XX			
PS	Claim 4; Page 74-76; 151pp; English.		
XX			
CC	The patent relates to polynucleotides encoding 35 plant transcription		
CC	factors which may be used to modify phenotype associated with a plant's		
CC	sugar sensing characteristics and increasing yield when their expression		
CC	level is altered. Sugars are central regulatory molecules that control		
CC	aspects of physiology, metabolism and development. Therefore the cDNAs		
CC	and proteins of the invention are useful for modifying the growth and		
CC	germination rates of plants, photosynthesis, glyoxylate metabolism,		
CC	respiration, starch and sucrose synthesis and degradation, pathogen		
CC	response, wounding response, cell cycle regulation, pigmentation,		
CC	flowering and senescence of plants and for modifying sink-source		
CC	relationships in seeds, tubers, roots, and other storage organs leading		
CC	to an increase in yield. The transcription factor polynucleotides and		
CC	polypeptides may be used to alter the structure and developmental		
CC	characteristics of plants such as soybean, wheat, corn, potato, cotton,		
CC	rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,		
CC	blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,		
CC	coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,		
CC	onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,		
CC	tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.		
CC	The present sequence is an Arabidopsis thaliana transcription factor.		
XX			
SQ	Sequence 532 AA;		

Query Match		99.9%;	Score 2754;	DB 22;	Length 532;
Best Local Similarity		99.8%;	Pred. No. 3.7e-256;		
Matches 531;		Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKRDRHHHHQDKKTMWNEEDDNGMDLAVLGYKVRSEMAVYDIAKIPGDALNQFAIDSASS	60		
DB	1	mkrdrhhhhqdkkttmmneeedngmdellavlgvkvrssemadvqakleqvmmnsnvq	60		
QY	61	EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDALNQFAIDSASS	120		
DB	61	eddlsqlatetvhynpaeltytwldsmldtnppssnaeydlkaipgdallnqfaidsass	120		
QY	121	SNQGGGDTYTNKRLKCSNGVWETTTATAESTRHVVLVDSQENGVRVHALLACAEAVQ	180		
DB	121	snqgggddtytnkrkcsngvvetttataestrhvvlvdsqengvrivhallacaeavq	180		
QY	181	KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQPIDHSLSDTLQ	240		
DB	181	kenltvaealvkqigflavsqigamrqvatyfaealarriyrlspsqpidhslsdtlqm	240		
QY	241	HFYETCPYLKFAHFTANQAILEAFQGGKKRVHVDFMSQGLQWALMALRPGGPPVF	300		
DB	241	hfyetcpylkfahftanqaileafqgkkrvhvdfmsqglqwpalmqalalrpggppvf	300		
QY	301	RLTGTGPPAPDNFDYLVHEVGCKLAHLAEAIHVEFEYRGFVANTLADLADSMLELRPSEIE	360		
DB	301	rltgtgppapdnfdylvhevgcklahlaeaihvefyrgfvantladldasmlrlpseie	360		
QY	361	SVAVNSVFELHKLGRPCAIDKVLGVNQIKPEITVVEQSNHNSPIFLDRFTESLHY	420		
DB	361	svavnsvfelhklgrpcaidkvlgvnmqikpeitvveqeshnspifldrfteshly	420		
QY	421	STLFDLSLEGVPSGQDKVMSEVILGQICNNVACDGPDRVERHETLSQWRNRFSGSAGFAAA	480		
DB	421	stlfdlslegvpsgqdkvmsevylgqicnnvacdgpdrverhetlsqwrnrfgsagfaaa	480		
QY	481	HIGSNFAKQASMLLALFNGEGYRYVEESDGLMLGWHTRP LIATSANKLSTN	532		
DB	481	higsnafkqasmllalfnggegyryveesdglmlgwhtrpliatsawklstn	532		
RESULT 3					
ID	AAE01907				
AC	AAE01907 standard; Protein; 532 AA.				
AC	AAE01907;				
DT	31-JUL-2001 (first entry)				
DE	Arabidopsis thaliana transcription factor, G308.				
KW	Transcription factor; biochemical characteristic; controlling element;				
KW	structural characteristic; developmental characteristic; gene therapy;				
KW	agricultural biotechnology; plant trait modification.				
OS	Arabidopsis thaliana.				
FH	Key Location/Qualifiers				
FT	Domain 270..274				
FT	/label= Conserved_domain				
XX	WO200136597-A1.				
XX	25-MAY-2001.				
XX	14-NOV-2000; 2000WO-US31344.				
XX	17-NOV-1999; 99US-0166228.				
XX	17-APR-2000; 2000US-0197899.				
XX	22-AUG-2000; 2000US-0227439.				
XX	(MEND-) MENDEL BIOTECHNOLOGY INC.				
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PA	(SAMA/) SAMAH R.				
PA	(PILG/) PILGRIM M.				
PA	(PINE/) PINEDA O.				
PA	(JIAN/) JIANG C.				
XX					
PI	Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R;				
PI	Pilgrim M, Pineda O, Jiang C;				
XX					
DR	WPI; 2001-335999/35.				
DR	N-PSDB; AAD05791.				
XX					
PT	Nucleic acids encoding plant transcription factor polypeptides, useful				
PT	for altering the biochemical characteristics of plants e.g. corn,				
PT	potato and cotton plants -				
XX					
PS	Claim 4; Page 114-115; 127pp; English.				
XX					
CC	The present sequence is Arabidopsis thaliana transcription factor,				
CC	G308, a homologue of G307. The transcription factor is used for altering				
CC	a plant's biochemical characteristics. The transcription factor may be				
CC	used to alter the structure and developmental characteristics of plants				
CC	such as soybean, wheat, corn, potato, cotton, rice, oilseed rape,				
CC	sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry,				
CC	strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber,				
CC	eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas,				
CC	peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato,				
CC	watermelon, rosaceous fruits and/or vegetable brassicas. Transcription				
CC	factors are key controlling elements of biological pathways and altering				
CC	expression levels of 1 or more transcription factors can change entire				
CC	biological pathways in an organism. Therefore manipulating transcription				
CC	factor levels in plants offers great potential in agricultural				
CC	biotechnology for modifying a plant's traits. Transcription factor cDNA				
CC	is useful in gene therapy.				
XX					
SQ	Sequence 532 AA;				
	Query Match	99.9%;	Score 2754;	DB 22;	Length 532;
	Best Local Similarity	99.8%;	Pred. No. 3.7e-256;		
	Matches 531;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKRDRHHHHQDKKTMWNEEDDNGMDLAVLGYKVRSEMAVYDIAKIPGDALNQFAIDSASS	60		
DB	1	mkrdrhhhhqdkkttmmneeedngmdellavlgvkvrssemadvqakleqvmmnsqv	60		
QY	61	EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKAIPGDALNQFAIDSASS	120		
DB	61	eddlsqlatetvhynpaeltytwldsmldtnppssnaeydikaipgdallnqfaidsass	120		
QY	121	SNQGGGDTYTNKRLKCSNGVWETTTATAESTRHVVLVDSQENGVRVHALLACAEAVQ	180		
DB	121	snqgggddtytnkrkcsngvvetttataestrhvvlvdsqengvrivhallacaeavq	180		
QY	181	KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQPIDHSLSDTLQ	240		
DB	181	kenltvaealvkqigflavsqigamrqvatyfaealarriyrlspsqpidhslsdtlqm	240		
QY	241	HFYETCPYLKFAHFTANQAILEAFQGGKKRVHVDFMSQGLQWALMALRPGGPPVF	300		
DB	241	hfyetcpylkfahftanqaileafqgkkrvhvdfmsqglqwpalmqalalrpggppvf	300		
QY	301	RLTGTGPPAPDNFDYLVHEVGCKLAHLAEAIHVEFEYRGFVANTLADLADSMLELRPSEIE	360		
DB	301	rltgtgppapdnfdylvhevgcklahlaeaihvefyrgfvantladldasmlrlpseie	360		
QY	361	SVAVNSVFELHKLGRPCAIDKVLGVNQIKPEITVVEQSNHNSPIFLDRFTESLHY	420		
DB	361	svavnsvfelhkllgrpcaidkvlgvnmqikpeitvveqeshnspifldrfteshly	420		

Qy 421 STLFDSLEGVPSGQKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNREGSAGFAAA 480
|||||
Db 421 stlfdslgvpvgqdkvmsevylgkqicnvvacdgpdrverhetlsqwrnrfgsagfaaa 480
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Qy 481 HIGSNAPKQASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLSTN 532
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Db 481 higsnaftqasmllalfnggegryveesdglmlgwhtrpliatssawklstn 532
|||||

RESULT 4
AAG38575
ID AAG38575 standard; Protein: 533 AA.
XX
AC AAG38575;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47610.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 10-JUN-1999; 99US-0140353.
PR 10-JUN-1999; 99US-0140354.
PR 10-JUN-1999; 99US-0140695.
PR 10-JUN-1999; 99US-0140823.
PR 10-JUN-1999; 99US-0140991.
PR 10-JUN-1999; 99US-0141287.
PR 10-JUN-1999; 99US-0141842.
PR 10-JUN-1999; 99US-0142154.
PR 10-JUN-1999; 99US-0142055.
PR 10-JUN-1999; 99US-0142390.
PR 10-JUN-1999; 99US-0142803.
PR 10-JUN-1999; 99US-0142920.
PR 10-JUN-1999; 99US-0142977.
PR 10-JUN-1999; 99US-0143542.
PR 10-JUN-1999; 99US-0143624.
PR 10-JUN-1999; 99US-0144005.
PR 10-JUN-1999; 99US-0144085.
PR 10-JUN-1999; 99US-0144086.
PR 10-JUN-1999; 99US-0144325.
PR 10-JUN-1999; 99US-0144331.
PR 10-JUN-1999; 99US-0144332.
PR 10-JUN-1999; 99US-0144333.
PR 10-JUN-1999; 99US-0144334.
PR 10-JUN-1999; 99US-0144335.
PR 10-JUN-1999; 99US-0144352.
PR 10-JUN-1999; 99US-0144632.
PR 10-JUN-1999; 99US-0144884.
PR 10-JUN-1999; 99US-0144814.
PR 10-JUN-1999; 99US-0145086.
PR 10-JUN-1999; 99US-0145088.
PR 10-JUN-1999; 99US-0145085.
PR 10-JUN-1999; 99US-0145087.
PR 10-JUN-1999; 99US-0145089.
PR 10-JUN-1999; 99US-0145192.
PR 10-JUN-1999; 99US-0145145.
PR 10-JUN-1999; 99US-0145218.
PR 10-JUN-1999; 99US-0145224.
PR 10-JUN-1999; 99US-0145276.
PR 10-JUN-1999; 99US-0145913.
PR 10-JUN-1999; 99US-0145918.
PR 10-JUN-1999; 99US-0145919.
PR 10-JUN-1999; 99US-0145951.
PR 10-JUN-1999; 99US-0146386.
PR 10-JUN-1999; 99US-0146388.
PR 10-JUN-1999; 99US-0146389.
PR 10-JUN-1999; 99US-0147038.
PR 10-JUN-1999; 99US-0147204.
PR 10-JUN-1999; 99US-0147302.
PR 10-JUN-1999; 99US-0147192.
PR 10-JUN-1999; 99US-0147260.
PR 10-JUN-1999; 99US-0147303.
PR 10-JUN-1999; 99US-0147416.
PR 10-JUN-1999; 99US-0147493.
PR 10-JUN-1999; 99US-0147935.
PR 10-JUN-1999; 99US-0148171.

CC SCARECROW-like (SCL) genes encoding proteins containing an amino acid
CC sequence similar to the sequence of MOTIF III (VHID) of Arabidopsis SCR
CC protein are disclosed. SCR and SCL genes are useful for producing
CC transgenic plants whose cell division is modified and root and/or stem
CC development and gravitropism of stem or hypocotyl is altered. Cell
CC division is increased or decreased in roots resulting in thicker or
CC thinner root development. The transgenic plants are useful for expressing
CC a gene of interest encoding a gene product that confers herbicide, salt,
CC pathogen or insect resistance in root or embryos and genes encoding
CC starch, lignin or cellulose biosynthesis in shoots. The SCR gene also
CC confers less susceptibility to lodging in the transgenic plants than a
CC wild-type plant. SCR gene sequences are also useful as molecular markers
CC for a quantitative trait e.g. root or gravitropism trait in molecular
CC breeding of crop plants.
xx
SQ Sequence 531 AA;

Query Match 99.3%; Score 2739.5; DB 21; Length 531;
Best Local Similarity 99.6%; Pred. No. 9.1e-255;
Matches 530; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Oy 1 MKRDHHHHQDKKTKMMNEEDGNGMDLLAVLGKVRSSMADVAOKLEOVMMNNVQ 60
Db 1 mkrdhhhhqdkktkmmneeedgngmdllavlgkvrssmadvakleievmmnnvq 60
Oy 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKALPGDAILNQFAIDSASS 120
Db 61 eddlsqlatetvhynpaelytwldsmldtnppssnaeydlkalpgd-ilnqfaidsass 119
Oy 121 SNQGGGGDTYTNKRKCSNGVWTTTATAESTRHVVLVDSQGVRLVHALLACAEAVQ 180
Db 120 snqggggdtytnkrkcsngvvettataestrhvvldvsgengvrlvhallacaeavq 179
Oy 181 KENITVAEALVKQIGFLAVSIOGAMRKVATYFAEALARRIYRLSPSOPIDHLSLSDTLQM 240
Db 180 kenitvaealvkqigflavsigamqvatyfaealarrlyrlspssqpsidhlsdltqm 239
Oy 241 HFYETCPYLKFAHTANQAILEAFQGGKRVHVDFSMSSQGLQWPAALALRPGGPPVF 300
Db 240 hfyetcpylkfahntanqaileafqgkkrvhvdfmsqglqwpalmqalalrpggppvf 299
Oy 301 RLITGGPPAPDNFDYLHEVGCKLAHLAEAIHVEFEYGFVANTLADLDASMLELRPSEIE 360
Db 300 rlitgppapdnfdylhevgcklhlaealhvefeygfvantladldasmllelrpseie 359
Oy 361 SVAVNSVPELHKLGRPGAIDKVLGVNQNQIKPEIFTVVEQSNHNSPIFLDRFTESLHY 420
Db 360 svavnsvelhklgrpgaiddkvlgvnnqikpeiftvveqsnhnspldrfteslhy 419
Oy 421 STLFDSEGVSPGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWNRNFGSAGFAAA 480
Db 420 stlfdsegvspgqdkvmsevylgkicnvvacdgpdrverhetlsqwnrnfsgafaaa 479
Oy 481 HIGSNAPQASMLALFNGEGYVEESDGLMLGHWTRPLIATSAWKLSTN 532
Db 480 higsnapqasmlallfnggegyrveesdgcmlgmghwtrpliatkawklstn 531

RESULT 6
AAG38576
ID AAG38576 standard; Protein; 518 AA.
AC AAG38576;
XX
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47611.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
xx

OS Arabidopsis thaliana.
xx
PN EPI033405-A2.
xx
PD 06-SEP-2000.
xx
PF 25-FEB-2000; 2000EP-0301439.
xx
xx 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 04-MAY-1999; 99US-0132048.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 25-MAY-1999; 99US-0135253.
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PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
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PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
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PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
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PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
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PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
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PR	07-OCT-1999;	99US-0158029.
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PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
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PR	21-OCT-1999;	99US-0160815.
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PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 96.8%; Score 2671; DB 21; Length 518;		
Best Local Similarity 100.0%; Pred. No. 3.5e-248;		
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1	mmneeeddgcgmdellavlgkvrsssemadvqkleglevmnsnvqeddisqlatetvhy 60
Qy	75	NPAELYTWLDSMLTDLPSPSSNAEYDLKAI PGDAILNQFAIDSSASSNOGGGDTYTTNK 134
Db	61	npaelytwldsmldclnppssnaeydikaipgdailnqfaidsassnqgggdttytnk 120
Qy	135	RLKCSNGVETTATTAESTRHRVILVDSQENGVRVLHALLACAEAVQKENLTVAEALVKQI 194
Db	121	rlkcsngvettataestrrhrvildsqengvrivhallacaeavqkenltvaealvkqi 180
Qy	195	GFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQMHFYETCPYLKTAHF 254
Db	181	gflavsqigamrkvatyfaealarriyrlspsqspidhslsdtlqmhfyetcpylktahf 240
Qy	255	TANQAIIEAFOGKKRVHVIDFSMSQGLQWPALMOALALRPGGPPVRLTGTIGPPAPDNFD 314
Db	241	tandqaiieafggkkrvrvldfsmssqglqwpalmqalalrpggppvrltgtigppapdnfd 300
Qy	315	YLHEVGCKLAHLAEIAHVEFEYRGFVANTLADLDASMLELRPSEIYESVAVNSVFLKLL 374
Db	301	ylhevckklahlaeiahvefeyrgfvantladldasmlelrpseiesvavnsvflkll 360
Qy	375	GRPGAIDKVLGVNQIKPEIFTVVQESNHNHSPILDRFTESLHYSTLFDLSLGVPSGQ 434

Db 361 grpgaidkvlgvnnqikpeifvteqesnhnspifldrfteslhyystlfdslgvpssgq 420
QY 435 DKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNREGSAGFAAAHIGSNAFKQASMLL 494
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QY 495 ALFNGGEGYRVEESDGCIMLGHWTPLIATSNAWKLSLN 532
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Db 481 alfnggegyrveesdgcimlgwhtrpliatsawklstn 518
RESULT 7
AAG38577
ID AAG38577 standard; Protein: 517 AA.
XX
AC AAG38577;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47612.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 08-APR-1999; 99US-0128714.
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PR 27-AUG-1999; 99US-0151065.
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PR 07-SEP-1999; 99US-0152363.
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PR 29-OCT-1999; 99US-0162142.

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Best Local Similarity 100.0%; Pred. No. 1e-247;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MNNEEDDNGMDLAVLGYKVRSEMDVAQKLEQLEVMMSNVQEDDLQSOLATETVHYN 75

Db 1 mmneeeddngmdellavlgkyvrsemdadvakleqlevmmsnvqeddlqsolatetvhn 60
QY 76 PAELYTWLDSMLTDLPSSNAEYDLKAIPGDALINQFAIDSASSNQGGGDTYTNKR 135
Db 61 paeltytwlidsmltdlppssnaeydlkaipgdalingfaidsassnqgggdttytnkr 120
QY 136 LKCSNGVYVETTATAESTRHVLDVDSQENGVRVLLHALLACAAEAVQKLENLTVAAALVKQIG 195
Db. 121 lkcsngyvettataestrhvldvdsqengvrvllhallaeeavqkenltvaalvkqig 180
QY 196 FLAVSQIGAMRKVATYFAEALARIYRLSPSQSIDHSLSDTLQMHFYETCPYLKFAHFT 255
Db 181 flavsqigamrkvatyfaealarriyrlspsqsidhslsdtlqmhfyetcpylkfahft 240
QY 256 ANQAILEAFQGGKRVHVDFDSMSQGLQWPAIMQALALRPGVPVRLTGIGPPAPDNFDY 315
Db 241 anqaileafggkkrvhvdfdsmsqglqwpaimqalalrpgppvrltgitgppapdnfdy 300
QY 316 LHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLELRPSETESVAVNSVFELHKLKG 375
Db 301 lhevgcklahlaeaihvefeyrgfvantladldasmllelrpseiesvavnsvfelhklkg 360
QY 376 RPGAIDKVLGVNQIKPEIFTVVEQESNHNPSIFLDRFTESLHYSTFLPSLSGVPSGQD 435
Db 361 rpgaiddkvlgvnqikpeiftvveqesnhnspifldrfteslhyystflpslsgvpsgqd 420
QY 436 KVMSEVYLGKQICNVACDGPDRVERHETLSQWNRNRFSGAGFAAAHTGSAFQAASMLLA 495
Db 421 kvmsevylgkqicnvacdgpdrverhetlsqwnrnfsgagfaahgtsafqaasmlla 480
QY 496 LFNGGEGYRVEESDGLMLGWHTRPLIATSARKLSTN 532
Db 481 lfnggegyrveesdglmlgwhtrpliatsarklstin 517
RESULT 8
AAE02560
ID AAE02560 standard; Protein; 587 AA.
XX
AC AAE02560;
XX
DT 10-AUG-2001 (first entry)
XX
DE A. thaliana transcription factor G308 homolog, G307.
KW Plant transcription factor; phenotype; sugar sensing characteristic;
KW transgenic plant; plant yield; growth; germination; photosynthesis;
KW glyoxylate metabolism; respiration; pathogen response; wounding response;
KW cell cycle regulation; pigmentation; flowering; senescence; physiology;
KW storage organ; metabolism.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT Domain 323..339
FT /note= "Conserved domain"
XX
PN W0200135725-A1.
XX
PD 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US31414.
XX
XX 17-NOV-1999; 99US-0166228.
PR 17-APR-2000; 2000US-0197899.
PR 22-AUG-2000; 2000US-0227439.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J.
PA (PINE/) PINEDA O.
PA (PILG/) PILGRIM M.

CC raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant,
CC grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers,
CC pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon,
CC rosaceous fruits and/or vegetable brassicas. Transcription factors are
CC key controlling elements of biological pathways and altering expression
CC levels of 1 or more transcription factors can change entire biological
CC pathways in an organism. Therefore manipulating transcription factor
CC levels in plants offers great potential in agricultural biotechnology
CC for modifying a plant's traits. Transcription factor cDNA is useful in
CC gene therapy.
XX
SQ Sequence 587 AA;

Query Match 79.4%; Score 2189.5; DB 22; Length 587;
Best Local Similarity 74.5%; Pred. No. 1e-201;
Matches 441; Conservative 39; Mismatches 43; Indels 69; Gaps 9;

Qy 1 MKRDHHH-----HH-----QDKKTMNNEEDGNGM-DELLAVLGKVRSEMA 43
Db 1 mkrdhhgfggrlshngtssssssiskdkmmvmkkeeoggmddellavlgkvrsema 60
Qy 44 DVAQKLEQLEVMNSVQEDDLSQATENVHYNPAELYTWLDSMLTDLNPP-----SSN-- 96
Db 61 evaileqleemsnvqdegishlatdvtvynpselyswldnmiselnpplpassngld 120
Qy 97 -----AEYDLKAIPGDAILNQFAIDSASSNSQGGGDTYTNKRKL-CSN-- 140
Db 121 pvlpspeicgfpasdydlkvpngaiyqfpaidsssn-----nqnrklscspsd 172
Qy 141 -----GVV-----ETTATAESTRHVVLVDQSQNGVRLVHALLACAEV 179
Db 173 smvtstgtgigvgitvtvttttttaaaestrsvilvdsgengvrlvhalmacaeai 232
Qy 180 QKENLTVAEALVKOIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSDIDHSLDTLQ 239
Db 233 qqnultiaaevlvgclawsqagamrkvatyfaealarriyrlspqngidhclsdltq 292
Qy 240 MHFYETCPYLKFAHFTANQALILEAFQCKRKHVHVIDFSMSQGLQWLPALMQALALRPGGPV 299
Db 293 mhfyetcpylkfahftanqaileafegkkrvhvidfsmqglqwpalmqalalreggppt 352
Qy 300 FRLTGIGPPAPDNFDYLHEVCCKLAHLAEATHVEFYRGFVANTLADLDASMLRLRSEI 359
Db 353 frltgigppapdnshlhevvgcklaqlaeaahvefyrgfvansladldasmlrlrpsdt 412
Qy 360 ESVAVNSVFELHKLGRPGADKVLGVVNOIKPEIFTVVEQESNHNPIFLDRFTESLHY 419
Db 413 eaavavnsfelhklgrpggiekvlgvvkqkpviftvveqeshngpvlfdrtfshy 472
Qy 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
Db 473 ystlfdlslegvpsgdkvmsevyilgkqicnvacegpdvrverheltsgnrgfsgslap 532
Qy 480 AHIGSNFAKQASMLLALFNGEGYRVESDCGLMGLWHTRPLIATSAWKLT 531
Db 533 ahlgsnfaqasmllsfnsgqgyrveesngclmglwhtrplittsawklst 584

RESULT 10
AAB31883
ID AAB31883 standard; Protein: 572 AA.
XX
AC AAB31883;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a wildtype GRAS protein.
XX
KW GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis;
KW plant development; dwarf plant; crucifer.
XX
OS Brassica napus.

XX WO200109356-A1.
PN
XX
PS
PD 08-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-FR02216.
XX
PR 02-AUG-1999; 99FR-0010023.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Renard M, Delourme R, Barret P, Brunel D, Froger N, Tanguy X;
XX
DR WPI; 2001-182964/18.
DR N-PSDB; AAF25480.
XX
PT New mutant nucleic acid encoding modified GRAS family protein, used to
PT produce dwarf transgenic plants -
XX
PS Example 1; Page 16-17; 28pp; French.
XX
CC The present sequence represents a wild type plant protein of the GRAS
CC family. The specification describes a mutant allele of the BZH gene,
CC which contains a G1695A mutation resulting in the mutation E546K in the
CC protein. GRAS proteins are transcription factors implicated in
CC regulation of the response to gibberellins and thus in control of
CC morphogenesis and plant development. The mutant GRAS protein is
CC used to produce dwarf plants, specifically crucifers. Dwarf plants may
CC be sown earlier (increasing nitrate accumulation without risking
CC excessive stem growth during winter), and have better resistance to
CC cold and lodging. They are also easier to harvest and allow for better
CC monitoring of the crop.
XX
SQ Sequence 572 AA;

Query Match 76.7%; Score 2114.5; DB 22; Length 572;
Best Local Similarity 73.6%; Pred. No. 1.6e-194;
Matches 430; Conservative 34; Mismatches 51; Indels 69; Gaps 9;

Qy 1 MKRDHHH-----HHQDK-----KTMNNEEDGNGMDELLAVLGKVRSE 41
Db 1 mkrdhhgfggrlshngtstssspavfgkdkmmvmkkee-----dellylgkvrse 56
Qy 42 MADVAQKLEQLEVMNSVQEDDLSQATENVHYNPAELYTWLDSMLTDLNPPSS----- 95
Db 57 maevalkleqletmngnaqeglahlatdvtvynpaeelyswldnmiselnpaattgsna 116
Qy 96 -NAEY-----DLKAIPGDAIL---NQPATDSASSNSQGGGDTYTNKRKLKCS 139
Db 117 lnpelnmnnnsfftggdlkaipgnavcrrsngfafavdss-----nkrklps 165
Qy 140 N-----GVVETT-TATAESTRHHVVLVDQSQNGVRLVHALLACAEVQKENTV 186
Db 166 sspdsmtvpspavigtvtvttestcrpildvdsgngvrlvhalmacaeavgsnlti 225
Qy 187 AEALVKOIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSDIDHSLDTLQMHFYETC 246
Db 226 aealvkqigflavsqagamrkvatyfaealarriyrlspqtdidhsltdlqmhfyetc 285
Qy 247 PYLKFAHFTANQALILEAFQCKRKHVHVIDFSMSQGLQWLPALMQALALRPGGPVFLRTGIG 306
Db 286 pylkfahftanqaileafegkkrvhvidfsmqglqwpalmqalalreggpvfrltgig 345
Qy 307 PPAPDNFDYLHEVCCKLAHLAEATHVEFYRGFVANTLADLDASMLRLRSETESVAVNS 366
Db 346 ppaadnsdhlhevvgcklaqlaeaahvefyrgfvansladldasmlrlrseteavavns 405
Qy 367 VFELHKLGRPGADKVLGVVNOIKPEIFTVVEQESNHNPIFLDRFTESLHYSTLFD 426
Db 406 vfelhklgrtggiekvlgvvkqkpviftvveqeshngpvlfdrtfshlystlfd 465
Qy 427 LEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNA 486

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Db 466 legapssqdkvmsevylgkqicnlvacegpdvrhetlsqwnrfsgsfapahlgnsa 525
QY 487 FKOASMLLALFNGEGYRVESDGLMLGWHTRLPFIATSAWKL 530
Db 526 fkgastlalfnggegyrveengclmshwtrplittsawkl 569

RESULT 11
AAB31884
ID AAB31884 standard; Protein: 572 AA.
XX
AC AAB31884;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a mutant GRAS protein.
XX
KW GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis;
KW plant development; dwarf plant; crucifer.
XX
OS Brassica napus.
XX
PN WO200109356-A1.
XX
PD 08-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-FR02216.
XX
PR 02-AUG-1999; 99FR-0010023.
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Renard M, Delourme R, Barret P, Brunel D, Froger N, Tanguy X;
XX
DR WPI; 2001-182964/18.
DR N-PSDB; AAF25481.
XX
PT New mutant nucleic acid encoding modified GRAS family protein, used to
PT produce dwarf transgenic plants -
PS Claim 4; Page 20-22; 28pp; French.
XX
CC The present sequence represents a mutant plant protein of the GRAS
CC family. The mutant allele of the BZH gene contains a G1695A mutation
CC resulting in the mutation E546K in the protein. GRAS proteins are
CC transcription factors implicated in regulation of the response to
CC gibberellins and thus in control of morphogenesis and plant development.
CC The mutant GRAS protein is used to produce dwarf plants, specifically
CC crucifers. Dwarf plants may be sown earlier (increasing nitrate
CC accumulation without risking excessive stem growth during winter), and
CC have better resistance to cold and lodging. They are also easier to
CC harvest and allow for better monitoring of the crop.
XX
SQ Sequence 572 AA;

Query Match 76.5%; Score 2110.5; DB 22; Length 572;
Best Local Similarity 73.5%; Pred. No. 3.9e-194;
Matches 429; Conservative 35; Mismatches 51; Indels 69; Gaps 9;

QY 1 MKRDHHH-----HHQDK-----KTMWNEEDGNGMDELLAVLGKVRSE 41
Db 1 mkrdlhfgqgnhtgsiagstspavfgdkmmmvkeed-----dellgvlgykvrse 56
QY 42 MADVAQKLEQLEVMWNVQEDDLSQLATETVHYNPALYTWLDSMLTDLNPPSS----- 95
Db 57 maevallkieqltmmnaqdgahlatdtvhympaelyswidmnlteipppaatgsna 116
QY 96 -NABY-----DLKAIPGDAIL---NOFAIDSASSNQGGGDTYTNKRLKCS 139
Db 117 lnpeinnnnnsfftgdllkaipgnavcrrsnqfafavsdss-----nkrllkps 165
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QY 140 N-----GVVETT-TATAESTHRVVLVDQSQNGVRLVHALACAAEVOKENLT 186
Db 166 sspdsmtspspagvigtvtvtvtestrplilvdsqngvrlvhalmaeavqssnltl 225
QY 187 AEAIVKQIGFLAVSQICAMRKVATYFAEALARRIYRSPSQSPIDHSLSDTLQWHFYETC 246
Db 226 aealvkqigflavsqagmrkvatyfaealartiyrlspptqgidhsldtlqmhfet 285
QY 247 PYLKFAHFTANOAILLEAFQGGKRVHVHIDFSMSQGLQWPAALMOALALRPGLPFLTGIG 306
Db 286 pylkfahftanqaileafegkkrvhvldfsmmqglqwpalmqalaleggppsflltgig 345
QY 307 PPAPDNFDYLHEYGCKLAHLAEAIHVEFEYRGVANTLADLDASMLERSEIESVAVNS 366
Db 346 ppaadnsdhlhevqcklaqlaeaihvefeyrgfvansladldasmlelrpseteavavns 405
QY 367 VFELHKLGRGAIDKVLGVVNOIKPEITVVEQESNHNPSIFLDRETSEHYSTLFD 426
Db 406 vfelhklgrtgglekvfgvkvkqkpvltvveqesnhngpvfldrfteshhyystlids 465
QY 427 LEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGSAGFAAAHIGSNA 486
Db 466 legapssqdkvmsevylgkqicnlvacegpdvrhetlsqwnrfsgsfapahlgnsa 525
QY 487 FKOASMLLALFNGEGYRVESDGLMLGWHTRLPFIATSAWKL 530
Db 526 fkgastlalfnggegyrveengclmshwtrplittsawkl 569

RESULT 12
AAB28574
ID AAB28574 standard; Protein: 587 AA.
XX
AC AAB28574;
XX
DT 09-FEB-2001 (first entry)
XX
DE Arabidopsis SCLa8.
XX
KW Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL;
KW transgenic plant; cell division; molecular marker; herbicide resistance;
KW salt resistance; pathogen resistance; insect resistance.
XX
OS Arabidopsis thaliana.
XX
PN WO200053723-A2.
XX
PD 14-SEP-2000.
XX
PF 07-MAR-2000; 2000WO-US05875.
XX
PR 10-MAR-1999; 99US-0265585.
XX
PA (UUNY ) UNIV NEW YORK STATE.
XX
PI Benfey PN, Di Laurenzio L, Wysocka-Diller J, Malamy JE, Pysh L;
PI Helariutta Y, Bruce W, Lim J;
XX
DR WPI; 2000-594315/56.
DR N-PSDB; AAC65291.
XX
PT Scarecrow gene useful for producing transgenic plants expressing genes
PT whose product increases starch, lignin or cellulose biosynthesis and
PT confers herbicide, pathogen or insect resistance -
XX
PS Claim 14; Fig 13; 200pp; English.
XX
CC The present sequence is given in a specification relating to the
CC structure and function of a regulatory gene, SCARECROW (SCR).
CC SCARECROW-like (SCL) genes encoding proteins containing an amino acid
CC sequence similar to the sequence of MOTIF III (WHIR) of Arabidopsis SCR
CC protein are disclosed. SCR and SCL genes are useful for producing
CC transgenic plants whose cell division is modified and root and/or stem
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development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistance in root or embryos and genes encoding starch, lignin or cellulose biosynthesis in shoots. The SCR gene also confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers for a quantitative trait e.g. root or gravitropism trait in molecular breeding of crop plants.

Sequence	587 AA;
SQ	

Query Match	74.7%	Score	2059.5	DB	21	Length	587
Best Local Similarity	70.8%	Pred. No.	3.3e-189				
Matches	419	Conservative	40	Mismatches	64	Indels	69
Gaps	9						
QY	1	MKRDRHH	-----HH-----	QDKKTKMMNEEDDNGCM	-DELLAVLGYKYRSESMA	43	
Db	1	mkrdrhhqfgrlnshgts	ssssssssiskdmmnmvkk	eedgggnmddellavlgkykrsema	60		
QY	44	DVAOKLEQLEVMNSVQ	EDDLSQLATETVHYNP	AEALYTLDLSMLTDLNP	---SSN---	96	
Db	61	evalklegletmmsna	qedgishlatdaahynp	elsylswldnmlielnpp	lpassngld	120	
QY	97	-----	---AEXDLKAIPGDA	ILNQPAIDSSASSNS	QGGGGDYTTNKR	140	
Db	121	pvlpspelcgfp	xsdydklvpixnalyqf	paiddsssn-----	-nqnkrkscspd	172	
QY	141	-----	---GW-----	ETTTATAESRPHVVL	VDSQBSNGVRLVH	179	
Db	173	smvtststgtqig	vgvgttttttttaae	srwlsvdsgqngvrlv	halmacaeai	232	
QY	180	QKENLTVAEALVQ	IGFLAVSQIGAMKRV	ATYFAEALARRIYR	USPQSPDHLSDTLQ	239	
Db	233	qgnnltaealvkg	iclavsgagcmkvat	yfaealarrtyr	lspbnqndhclsdtlq	292	
QY	240	MHFYETCPYLKFA	HTTANOATLEAFQCK	RVRHVHIDFSMSQ	LOWPALMQALALR	299	
Db	293	mhfyetcpylk	hftanqaileafegk	rvrhvhdifsmgql	qvpalmqalalreg	352	
QY	300	FRLTGIGPPADPN	FDYLHHEWGCKLAH	LAETHVEFYRGFV	ANTLADLDSMLER	359	
Db	353	frltgigppadnsd	hhevgcklaqlaeai	lhvefyrgfvansla	dlidsamlelrpsdt	412	
QY	360	ESVAVNSVEELHKL	LRPGATDKVLGVV	NQIKPEITFTVQES	NHNSPIFLDR	419	
Db	413	esavnsvfehlkl	lgrxgglekvlgvv	kgdqtgafhwxr	qegpnhngpgf	472	
QY	420	YSTLFDLSLEG	VPSGQDRKVMSEV	YLKGQICNVVACD	GGDPDRVERHET	479	
Db	473	ystxfdsleg	xpsnsgdklmsey	ylgxcnlvacegdp	rverhetlsqwnr	532	
QY	480	AHIGSNAPKQAS	MLLALFNGEGYRV	ESDGCMLGWH	TRPLIATS	531	
Db	533	ahigsnafkasm	llswfngsggyrvee	ngcmlgwhtrp	littskawslat	584	

RESULT	13	
XX	AA02541	
ID	AA02541	standard; Protein; 630 AA.
XX	XX	
XX	AA02541	
XX	XX	
DT	16-JUL-1999	(first entry)
XX	XX	
DE	DE	Protein encoded by maize lal genomic clone sequence.
XX	XX	
KW	KW	Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW	KW	antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
XX	XX	paclobutrazol; maize.
XX	XX	

Zea mays.

XX PN WO9909174-A1

XX
PD
25-FEB-1999.XX
PF
07-AUG-1998;XX
PR 13-AUG-1997: 97GB-0017192XX
PA (PLAN-) PLANT BIOSCIENCE LTDXX
PI
Harberd NP, Peng J, Richards DE:

XX
DR WPT: 1999-181040/15.

DR N-PSDB; AAX36280.
XX

PT New *Triticum aestivum* polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

PS Disclosure; Fig 9b; 88pp; English.

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in *Triticum Aestivum*, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the maize 1a1 genomic clone sequence.

AA	Sequence	630 AA;
SQ		

Query Match	58.1%	Score	1602.5	DB	20	Length	630
Best Local Similarity	54.0%	Pred. NO.	3.8e-145				
Matches	344	Conservative	68	Mismatches	106	Indels	119
						Gaps	15

QY 1 MKRDHHHHHQD-----KKTMM-----NEEDDNGMDELLAVLGYKVRSSEM 42

Db 1 mkre---yqdagggsgdmgsskdkmmaaaagageqeeed---vdellaalgykvrssdm 53

QY 43 ADVAQKLEQLEVM-----SNQEDD--LSQLATETVHYNPAELYTWLDSMLTDLNPP 93

54 advaqkleglemamqmqvqqaaqataddqfvshlatdvtvhynpsdlsswvesmlselnap 11

94 -----SSNAEYDLKAIPGDAILLNOFAT 11

Db 114 paplppatpaprlastssstvtssaaaaagqvfdlppavdsssstvalkpip-----spvaa 16

0Y 116 DSASSSNOG-----GGDVTYTNKRI.KCSNG-----VVE-----TTTATAESTR-- 15

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160 nnaadnnetdcaarankrmrtacactcccccccccsmddqrrtrccvuucaannatcaccaaaaanaaa::

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00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

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QY 332 VEFYRFGVANTLADLASMLELR-----PSEIESVAVNSVFELHKLGRGAIKRVLGV 387
Db 409 vdfyrgivaatladeplfmqlpegddtdddepevianvsvfelhrllaqgalekvlgvt 468
QY 388 NOIKPEITVVEESNHNPSIFLDRFTESLHYSTLFDLSLEGVPSGQ----- 434
Db 469 ravprlvvveqeanhnsgrtldfreslhysscmfsllegagsgsgsdaspaaagg 528
QY 435 -DKVMSEYVLGKQICNVVACGPDPRVERHETLSQWRNRFSGAGFAAAHIGSNAFKQASML 493
Db 529 lqdvmsvylgrqicnvvacageaerhetlqgwrslgsgfapvhlgsnqaykqastl 588
QY 494 LALFNGGEGYRVEESDGLMLGWHTRPLIATSANKLS 530
Db 589 lalfaggdyrveekdglctlgwhtrplatsawrva 625

RESULT 14
AAV02540
ID AAV02540 standard; Protein: 623 AA.
XX AC AAV02540;
XX DT 16-JUL-1999 (first entry)
XX DE Protein encoded by wheat Rht clone 5a1 genomic sequence.
XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
XX KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
XX KW paclobutrazol.
XX OS Triticum aestivum.
XX PN WO9909174-A1.
XX PD 25-FEB-1999.
XX PE 07-AUG-1998; 98WO-GB02383.
XX PR 13-AUG-1997; 97GB-0017192.
XX PA (PLAN-) PLANT BIOSCIENCE LTD.
XX PI Harberd NP, Peng J, Richards DE;
XX DR WPI; 1999-181040/15.
XX DR N-PSDB; AAX36279.
XX PT New Triticum Aestivum polynucleotides - encode a polypeptide which
XX PT provides inhibition of the growth of plants, which inhibition is
XX PS antagonised by gibberellin, used to confer a dwarf phenotype
XX PS Disclosure; Fig 8b; 88pp; English.
XX CC The specification describes polypeptides encoded by the Rht gene (and
XX CC its homologues) that, when expressed in Triticum Aestivum, inhibit
XX CC growth of the plant. This growth inhibition is antagonised by
XX CC gibberellin. The products can be used to provide Rht expression in
XX CC plants, conferring a dwarf phenotype on a plant which is correctable
XX CC by treatment with gibberellin. In addition, the products can be
XX CC used to produce Rht mutant plants which are dwarfed compared with
XX CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
XX CC may be made by knocking out Rht or the relevant homologous gene in
XX CC the plant of interest. Plants may be made which are resistant to
XX CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
XX CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
XX CC dwarf but let crop plants grow tall. The present sequence is encoded by
XX CC the wheat Rht clone 5a1 genomic sequence.
XX SQ Sequence 623 AA;

Query Match 57.88; Score 1594; DB 20; Length 623;

Best Local Similarity 54.3%; Pred. No. 2.5e-144;
Matches 332; Conservative 71; Mismatches 106; Indels 102; Gaps 11;

QY 11 DKKTMMNEEDGNGMDELLAVLGKVFSSSEMADVAAKLEQLEVM-----SNVQEDD- 63
Db 22 edkmvsaageevdellaalgkykrasmdadvakleqlmangmgvgagaapdds 81
QY 64 -LSLATETVHYNPAELYTWLDSMLTDLNPP-----NQFAIDSASSNQGGGDT 93
Db 82 fathlatvtvnyptdlsswvesmlseinaappplppapqinaaststvtsggyfdlpp 141
QY 94 ---SSNAEYDLKAIP-----GDAIL----- 129
Db 142 svdsssiyalrppspagatapadlsadvrdpkrmttggssstsssssssggg--- 198
QY 130 YTTNKLKCSNGVVE-----TTTATAESTRHWLVDSOENGVRVLVHALLACAEAVOKENL 184
Db 199 -----arssvveappvaaaanataplvvvvdtqeaagirlvhallacaeavqqenl 250
QY 185 TVAEALVKQIGFLAVSQIGAMRKVATYFAEALARIYRL--SPSQSPIDHLSLDTLOMHF 242
Db 251 saaealvkqipllaasqggamrkvaayfgealarrrvfrpqpdsllidaafadilhahf 310
QY 243 YETCPYLKFAHFTANQAILFAFGKKRVHVIDFSQSLQWLPALMQALALRPGGPPVRL 302
Db 311 yescpylkfahftanqailfaagcrrvvhvdfgkqgmqpallqalalrpggppsfri 370
QY 303 TGICPPAPDNFDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLDASML----ELRPS- 357
Db 371 tgvppppdcdalqgvqwklaqfahtirvdfgyrglvaatladielpmlpegeedpne 430
QY 358 EIESVAVNSVFELHKLGRGAIKRVLGVVNOIKPEITVVEESNHNPSIFLDRFTESL 417
Db 431 epeviavnsvfemhrlaqpqalekvigtvzavrprlvvveqeanhnsgrtldfresl 490
QY 418 HXYSTLFDLSLE-----VPSGODKVMSEVYLGKQICNVVACDGPDRV 459
Db 491 hyystmfdsllegsgsgsgpsevsgaaagtdqvmsevygrqicnvvacageaert 550
QY 460 ERHETLSQWRNRFSGAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEESDGLMLGWHTR 519
Db 551 erhetlqgwrnrlgnagfetvhlgsnqaykqastllalfaggdykveeegcltligwhtr 610
QY 520 PLIATSANKLS 530
Db 611 pliatasawrla 621

RESULT 15
AAV02539
ID AAV02539 standard; Protein: 425 AA.
XX AC AAV02539;
XX DT 16-JUL-1999 (first entry)
XX DE Protein encoded by the wheat Rht clone C15-1 cDNA sequence.
XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
XX KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
XX KW paclobutrazol.
XX OS Triticum aestivum.
XX PN WO9909174-A1.
XX PD 25-FEB-1999.
XX PE 07-AUG-1998; 98WO-GB02383.
XX PR 13-AUG-1997; 97GB-0017192.
XX PA (PLAN-) PLANT BIOSCIENCE LTD.

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XX Harberd NP, Peng J, Richards DE;
PI WPI: 1999-181040/15.
DR N-PSDB; AAX36278.
XX
XX New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
XX Disclosure; Fig 7b; 88pp; English.
XX
XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence is encoded by
CC the wheat Rht clone C15-1 cDNA sequence.
XX
SQ Sequence 425 AA;

Query Match 49.9%; Score 1375; DB 20; Length 425;
Best Local Similarity 64.4%; Pred. No. 1.6e-123;
Matches 271; Conservative 46; Mismatches 74; Indels 30; Gaps 5;

QY 140 NGVVE-----TTTAASTRHVVLVDSQENGVRVLVHALLACAAVQKENTLVAEALVKQI 194
Db 3 ssvveaappvaaaanataplpvvvvtqdagirivhallacaeavqgnlsaaealvkqi 62

QY 195 GLAVSQIGAMRKVATFAEALARRIYRL--SPSQSPIDHSLSDTLQMHFYETCPYLKFA 252
Db 63 pllaasggamrkvaayfgealarvfrfpdpdsslldaafadllhahfyescpylkfa 122

QY 253 HFTANQALEAFQSKKRVRHVVDIFSOGLOPDMQALALRPGGPPVFRLTGIGPPAPDN 312
Db 123 hftanqalleafagcrrrvhvvdfigkgmqwpallqalalrpggppsfrltgvgppqpd 182

QY 313 FDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLASML---ELRPS-EIESVAVNSV 367
Db 183 tdaigqvgwklaqfahtirvofqrgivaacladlepfmqlqgegedpneepeviavnsv 242

QY 368 FELHKLGRGAIDKVLGVVWQIKPEFTVVEQESNNHNSPIFLDRFTESLHYSTFLDLSL 427
Db 243 femhrliaqpgalekvgtvavtrivtvegeanhnsgtfldrfteslhystmfdsl 302

QY 428 EG-----VPSGQDKVMSEYLGKQICNVVACDGPDRVERHETLSQWR 469
Db 303 eggssgggppsevssgaaapaagtdqvmsevylgqicnvvaccegaerterhetlgqr 362

QY 470 NREGSFAAAHIGSNAPKQAMLLALFNNGEGYRVESDGCLMLGWHTRPLIATSARKL 529
Db 363 nrlgnagfetvhlgsnaykqastllaifagggdykveekgccltlgwhtrpliatsawl 422

QY 530 S 530
Db 423 a 423
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Job time: 205 sec

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